

Genomic and Phenotypic Characterization of Yeast Biosensor for Deep-space Radiation. Diana B. Marina, Sergio Santa Maria and Sharmila Bhattacharya. NASA Ames Research Center, Moffett Field, CA.

The BioSentinel mission was selected to launch as a secondary payload onboard NASA Exploration Mission 1 (EM-1) in 2018. In BioSentinel, the budding yeast *Saccharomyces cerevisiae* will be used as a biosensor to measure the long-term impact of deep-space radiation to living organisms. In the 4U-payload, desiccated yeast cells from different strains will be stored inside microfluidic cards equipped with 3-color LED optical detection system to monitor cell growth and metabolic activity. At different times throughout the 12-month mission, these cards will be filled with liquid yeast growth media to rehydrate and grow the desiccated cells. The growth and metabolic rates of wild-type and radiation-sensitive strains in deep-space radiation environment will be compared to the rates measured in the ground- and microgravity-control units. These rates will also be correlated with measurements obtained from onboard physical dosimeters.

In our preliminary long-term desiccation study, we found that air-drying yeast cells in 10% trehalose is the best method of cell preservation in order to survive the entire 18-month mission duration (6-month pre-launch plus 12-month full-mission periods). However, our study also revealed that desiccated yeast cells have decreasing viability over time when stored in payload-like environment. This suggests that the yeast biosensor will have different population of cells at different time points during the long-term mission. In this study, we are characterizing genomic and phenotypic changes in our yeast biosensor due to long-term storage and desiccation. For each yeast strain that will be part of the biosensor, several clones were reisolated after long-term storage by desiccation. These clones were compared to their respective original isolate in terms of genomic composition, desiccation tolerance and radiation sensitivity. Interestingly, clones from a radiation-sensitive mutant have better desiccation tolerance compared to their original isolate without losing radiation sensitivity. We employed Next-Generation Sequencing technology to better understand this phenotypic variation. Current effort is focusing on the analysis of high-throughput sequencing data to look for genomic changes in these reisolated clones compared to their original isolate.

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